

# SURFACE-MEDIATED ACTIVATION OF BLOOD COAGULATION (INTRINSIC SYSTEM)

11 969863

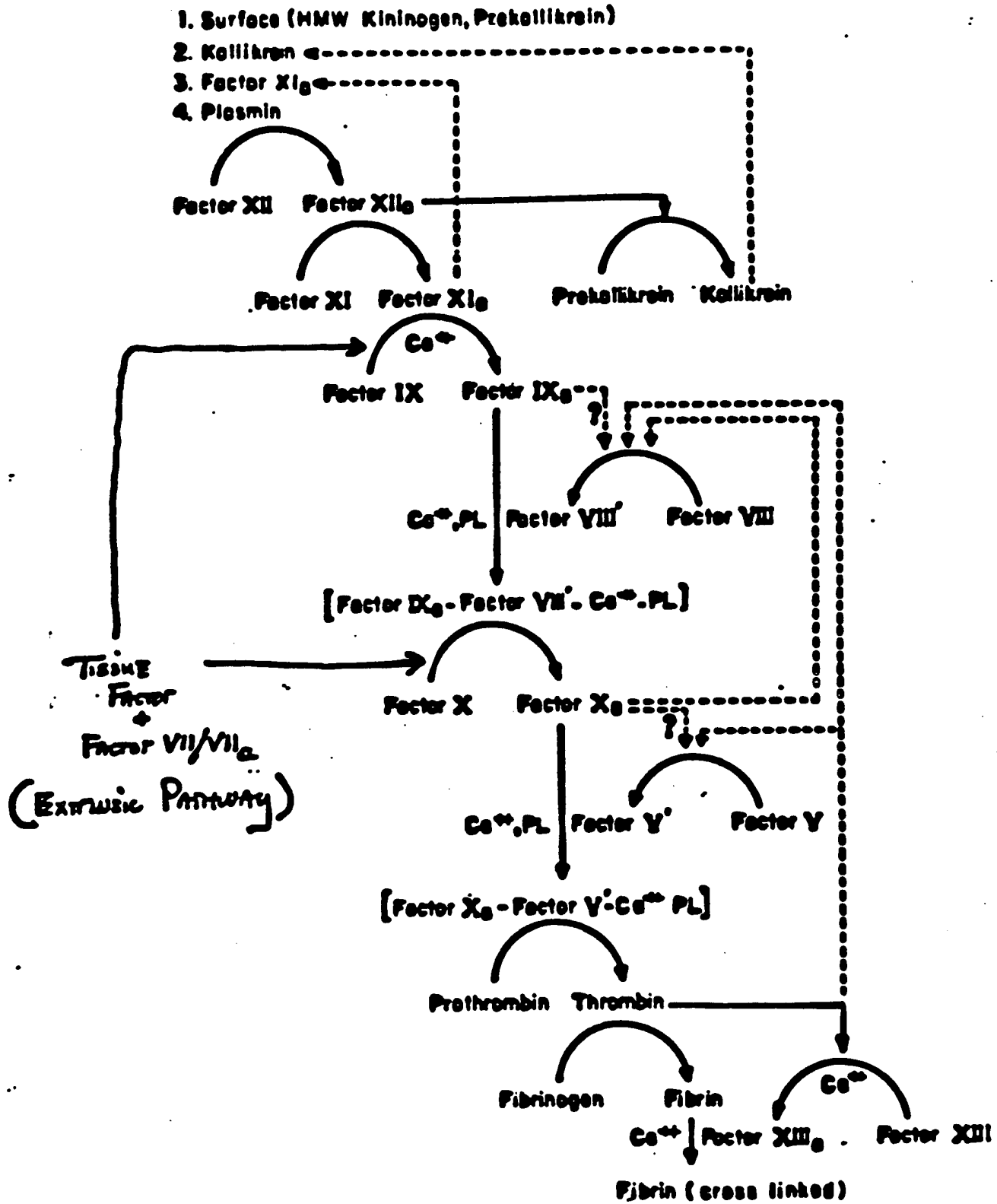
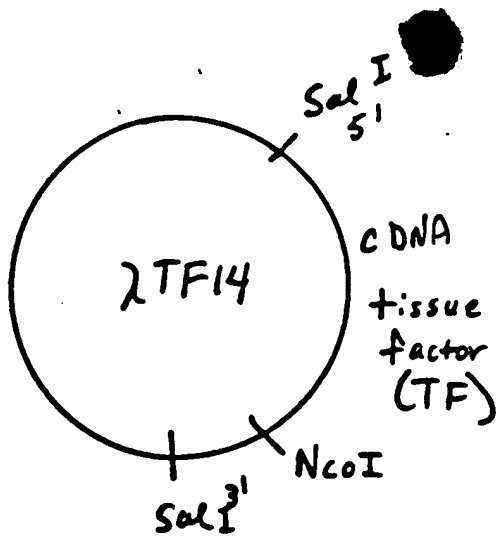


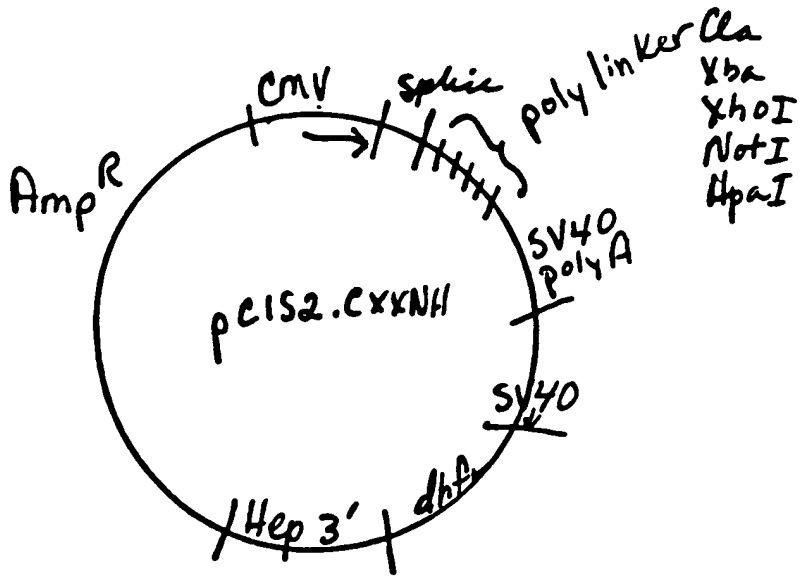
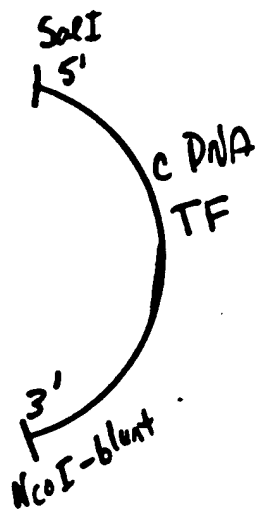
FIGURE 1

FIGURE 4

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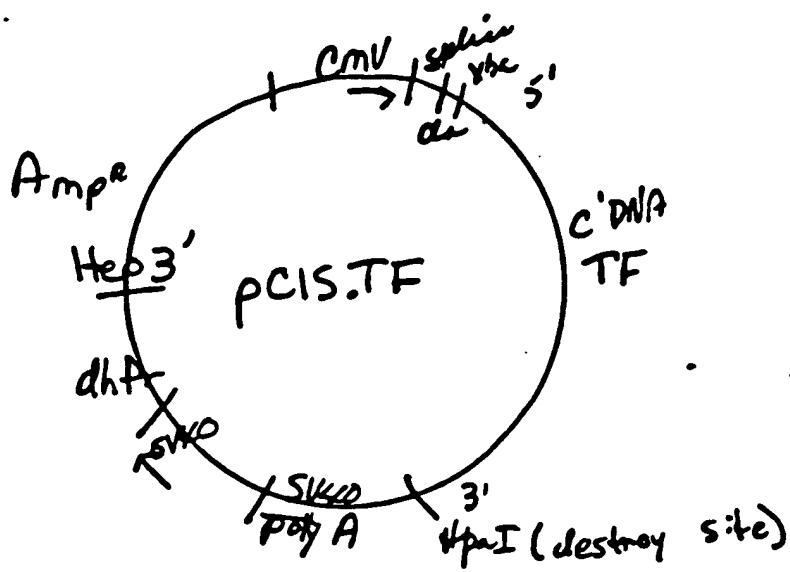


1. cut with NcoI
2. fill in with Klenow  
+ 4 dNTP
3. cut with Sal (TCGA)
4. isolate 1232 bp fragment



1. cut with XhoI (TCGA)  
and HpaI
2. gel purify

ligation



1 CTCGCACTCCCTCTGCGCGGCCACGGGCGCCTTCAGCCCAACCTCCCCAGCCCCACGGGCGCCACGGAACCCGCTCGATCTCGCCGCCAACTGGTAGAC  
100 ATG GAG ACC CCT GCC TGG CCC CGG GTC CCG CGC CCC GAG ACC GCC GTC GCT CGG ACG CTC CTG CTC GGC TGG GTC  
-32 Met Glu Thr Pro Ala Trp Pro Arg Val Pro Arg Pro Glu Thr Ala Val Ala Arg Thr Leu Leu Leu Gly Trp Val  
175 TTC GCC CAG GTG GCC GGC GCT TCA GGC ACT ACA AAT ACT GTG GCA GCA TAT AAT TTA ACT TGG AAA TCA ACT AAT  
-7 Phe Ala Gln Val Ala Gly Ala Ser Gly Thr Thr Asn Thr Val Ala Ala Tyr Asn Leu Thr Trp Lys Ser Thr Asn  
250 TTC AAG ACA ATT TTG GAG TGG GAA CCC AAA CCC GTC AAT CAA GTC TAC ACT GTT CAA ATA AGC ACT AAG TCA GGA  
19 Phe Lys Thr Ile Leu Glu Trp Glu Pro Lys Pro Val Asn Gln Val Tyr Thr Val Gln Ile Ser Thr Lys Ser Gly  
325 GAT TGG AAA AGC AAA TGC TTT TAC ACA ACA GAC ACA GAG TGT GAC CTC ACC GAC GAG ATT GTG AAG GAT GTG AAG  
44 Asp Trp Lys Ser Lys Cys Phe Tyr Thr Thr Asp Thr Glu Cys Asp Leu Thr Asp Glu Ile Val Lys Asp Val Lys  
400 CAG ACG TAC TTG GCA CGG GTC TTC TCC TAC CCG GCA GGG AAT GTG GAG AGC ACC GGT TCT GCT GGG GAG CCT CTG  
69 Gln Thr Tyr Leu Ala Arg Val Phe Ser Tyr Pro Ala Gly Asn Val Glu Ser Thr Gly Ser Ala Gly Glu Pro Leu  
475 TAT GAG AAC TCC CCA GAG TTC ACA CCT TAC CTG GAG ACA AAC CTC GGA CAG CCA ACA ATT CAG AGT TTT GAA CAG  
94 Tyr Glu Asn Ser Pro Glu Phe Thr Pro Tyr Leu Glu Thr Asn Leu Gly Gln Pro Thr Ile Gln Ser Phe Glu Gln  
550 GTG GGA ACA AAA GTG AAT GTG ACC GTA GAA GAT GAA CGG ACT TTA GTC AGA AGG AAC AAC ACT TTC CTA AGC CTC  
119 Val Gly Thr Lys Val Asn Val Thr Val Glu Asp Glu Arg Thr Leu Val Arg Arg Asn Asn Thr Phe Leu Ser Leu  
625 CGG GAT GTT TTT GGC AAG GAC TTA ATT TAT ACA CTT TAT TAT TGG AAA TCT TCA AGT TCA GGA AAG AAA ACA GCC  
144 Arg Asp Val Phe Gly Lys Asp Leu Ile Tyr Thr Leu Tyr Tyr Trp Lys Ser Ser Ser Ser Gly Lys Lys Thr Ala  
700 AAA ACA AAC ACT AAT GAG TTT TTG ATT GAT GTG GAT AAA GGA GAA AAC TAC TGT TTC AGT GTT CAA GCA GTG ATT  
169 Lys Thr Asn Thr Asn Glu Phe Leu Ile Asp Val Asp Lys Gly Glu Asn Tyr Cys Phe Ser Val Gln Ala Val Ile  
775 CCC TCC CGA ACA GTT AAC CGG AAG AGT ACA GAC AGC CCG GTA GAG TGT ATG GGC CAG GAG AAA GGG GAA TTC AGA  
174 Pro Ser Arg Thr Val Asn Arg Lys Ser Thr Asp Ser Pro Val Glu Cys Met Gly Gln Glu Lys Gly Glu Phe Arg  
850 GAA ATA TTC TAC ATC ATT GGA GCT GTG GTA TTT GTG GTC ATC ATC CTT GTC ATC ATC CTG GCT ATA TCT CTA CAC  
219 Glu Ile Phe Tyr Ile Ile Gly Ala Val Val Phe Val Val Ile Ile Leu Val Ile Ile Leu Ala Ile Ser Leu His  
925 AAG TGT AGA AAG GCA GGA GTG GGG CAG AGC TGG AAG GAG AAC TCC CCA CTG AAT GTT TCA TAA AGGAAGCACTGTTGG  
244 Lys Cys Arg Lys Ala Gly Val Gly Gln Ser Trp Lys Glu Asn Ser Pro Leu Asn Val Ser End  
1003 AGCTACTGCAAAATGCTATATTGCACTGTGACCGAGAACCTTTAAGAGGATAGAATACATGGAACGCAAAATGAGTATTTTCGGAGCATGAAGACCCCTGGAG  
1103 TTCAAAAACTCTTGATATGACCTGTTATTACCATTAGCATTCTGGTTTTGACATCAGCATTAGTCACTTTGAAATGTAACGAATGGTACTACAACCAAT  
1203 TCCAAGTTTTAATTTTTAACACCATGGCACCTTTTGACATAACATGCTTTAGATTATATATTCGCACTCAAGGAGTAACAGGTCGTCCAAGCAAAAA  
1303 CAAATGGGAAAAATGTCTTAAAAAATCCTGGGTGGACTTTTGAAAAGCTTTTTTTTTTTTTTTTTTTGAGACGGAGTCTTGCTCTGTTGCCAGGCTGGA  
1403 GTGAGTAGCACGATCTCGGCTCACTGCACCTCCGCTCTCGGGTTCAAGCAATTGTCTGCCTCAGCCTCCCGAGTAGCTGGGATTACAGGTGCACCT  
1503 ACCACACCAAGCTAATTTTTGTATTTTTTAGTAGAGATGGGGTTTACCATCTTGCCAGGCTGGTCTTGAATTCCTGACCTCAGTTGATCCACCCACCT  
1603 TGGCTCCCAAAGTGTAGTATTATGGGCGTGAACCAACATGCCAGCCGAAAAGCTTTTGAGGGGCTGACTTCAATCCATGTAGGAAAGTAAATGGA  
1703 GGAATTTGGGTGATTTCTAGGACTTTTCTAACATATGTCTATAATATAGTGTGTTAGGTTCTTTTTTTTTTTCAGGAATACATTTGGAATTCAAAACAA  
1803 TGGCAAACTTTGTATTAATGTGTTAAGTGCAAGGACATTGGTATTCTGGGCACCTTCTTAATATGCTTTACAATCTGCACTTTAACTGACTTAAGTGGC  
1903 ATTAACATTTGAGAGCTAACTATATTTTATAAGACTACTATACAACTACAGAGTTTATGATTTAAGGTAAGTAAAGCTTCTATGGTTGACATTGTAT  
2003 ATATAATTTTTTAAAAAGGTTTTCTATATGGGGATTTTCTATTTATGTAGGTAATATTGTTCTATTTGTATATATTGAGATAATTTATTTAATATACTTT  
2103 AAATAAAGGTGACTGGGAATTGTTA<sub>n</sub>

[illegible]

1001 GAGCTACTG CAATGCTAT ATTGCACTGT GACCGAGAC TTATAGAGG <sup>nl</sup> ATAGATATCA TCGAAGCGA ATAGATAT TCGAAGCATG AGACCTCTG <sup>nl</sup> GGTGATGAG GTTATAGATA TACGCTGACA CTGCTCTCTG AATATCTCC TATCTATCT ACCCTGCGT TATCTATCA AACCTGCTG TCTGCGAGC  
 1101 AGTTCANAA ACCTTGATA TGACCTGTA TTACCATAG CATCTGCTT <sup>bs</sup> TTGACATG CATTAATGCT TTGAATGT AACGATGT ACTACACCA TCAAGTTT TCAATCAT ATGCAATAT ATGCTATG GTACACCAA ACTGATGT GTATCATG AACCTTACA TTCTTACA TCAATGCT  
 1201 ATTGCACTT TTAATTTTA ACACCATGCT ACCCTTGCA CATACATG TTATGATAT ATATCGCGA CTACAGAGT AACCATGCT TCGACCAA TACGCTCA AATTAATAT TGCTGACG TCAATATCA AATCTATCA TATATGCGT CATCTCTCA TATCTCTCA TTCTCTCA TCTGCTCA AGCTGCGC  
 1301 AACAAATGG AATATGCTT AAAAAATCT GGTGCACTT TTGAATGCT TTTTCTT TTTTCTT AGACGAGT TTCTCTGT GCCGAGCTG TCTTACCT TTATACAAA TTTTACGA CCCACTGAA ACTTCTCA AAAAAAA TCTGCTCTG AACGACCAA CGGCTCGAC  
 1401 GAGTGCAGTA GCACGATCTC GGTCTACTG ACCCTGCTG TCTGCGCTC AATCATGCT AACGATGCT CTGCTCTAG CTCCGAGTA CAGGCTGGA CTACGCTAT CGTCTGAGG CGAGTACG TCGAGCGAG AGACCGCAG TTGCTTACA GAGGAGCTG GAGGCTCAT CGACCTTAT CTCCAGCGT  
 1501 CTACACACG AGCTAATTT TTGATTTT TAGTAGAGAT GGGCTTCTC CATCTGCTC GATCTGGCC AGCTGCTT TGAATCTG ACTCTAGT ATCCACCGC CATGCTGCT TTGATTTAA AATATATA ATCATCTCA CCCAATGCT GTAGAACCG TCGACACCA ACTATAGC TGAATCTAG TAGTGGCTG  
 1601 CTGACCTCC CAATGCTTA GTATATGCG CTGACACG CAGACCGC GGAATGCT TTGAGCGCT GACTTCATC CATATGCA AGTAATGCG GACCGGAGG GTTACAGAT CATATATGCC GCACTGCTG GTAGCGCTG GCTTCTCA AATCTCCCA CTGAGTTAG GTACTCTT TCAATTAC  
 1701 AACGAATG CTGCACTTC TACGCTTT CTATCATAG TCTATATAT AGCTTACG TTCTTTT TTTCAGAT ACATTCGA ATTCAACA TCTCTTAC CACGTAAAG ATCTGAAA CATCTATC ACATATATA TCAAAATG AAAAAAA AATCTCTA TGTAACTT TAACTTCT  
 1801 ATTGCAAC TTGTATTA TGTGTAGT GAGAGAGCA TTGCTATCT GGGACCTTC CTATATGCT TTACATGCT GACTTACT GACTTATG TACCGCTTG AACATTAAT ACATATCA CTGCTCTG AACATAGA CCCCGGAG GATTATGA ATCTTACG GTAAATGA CTGATTCG  
 1901 GCAATTAACA TTGAGAGT AACTATAT TTATAGACT ACTATACAA CTACAGACT TATGATTA GATCTCTA ATCTAAT CTATGATTT CGAATATC CAAGATAC ACTGTACA CGTATTTG AACTCTCA TGTATTA AATCTCTA TATATGTT GATCTCTA ATCTAAT CTATGATTT CGAATATC CAAGATAC ACTGTACA  
 2001 ATATATAT TTTAATAAG GTTCTTATA TCGCATTT CTATTATGT AGCTAATTT GTCTATTT TATATATGA GATAATTA TTAATATC ATATATAT AATATTTT CAATAATAT ACCCTTAA GATAATTA TCAAT-TTA CAGATTAAC ATATATAT CTATTATA ATATATGA  
 2101 TTAATTAAG GTCACTGCA ATTGTA AATTATTC CACTGACCT TACCAAT  
 2length: 2137

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Fig. 5

